

FIG. 1

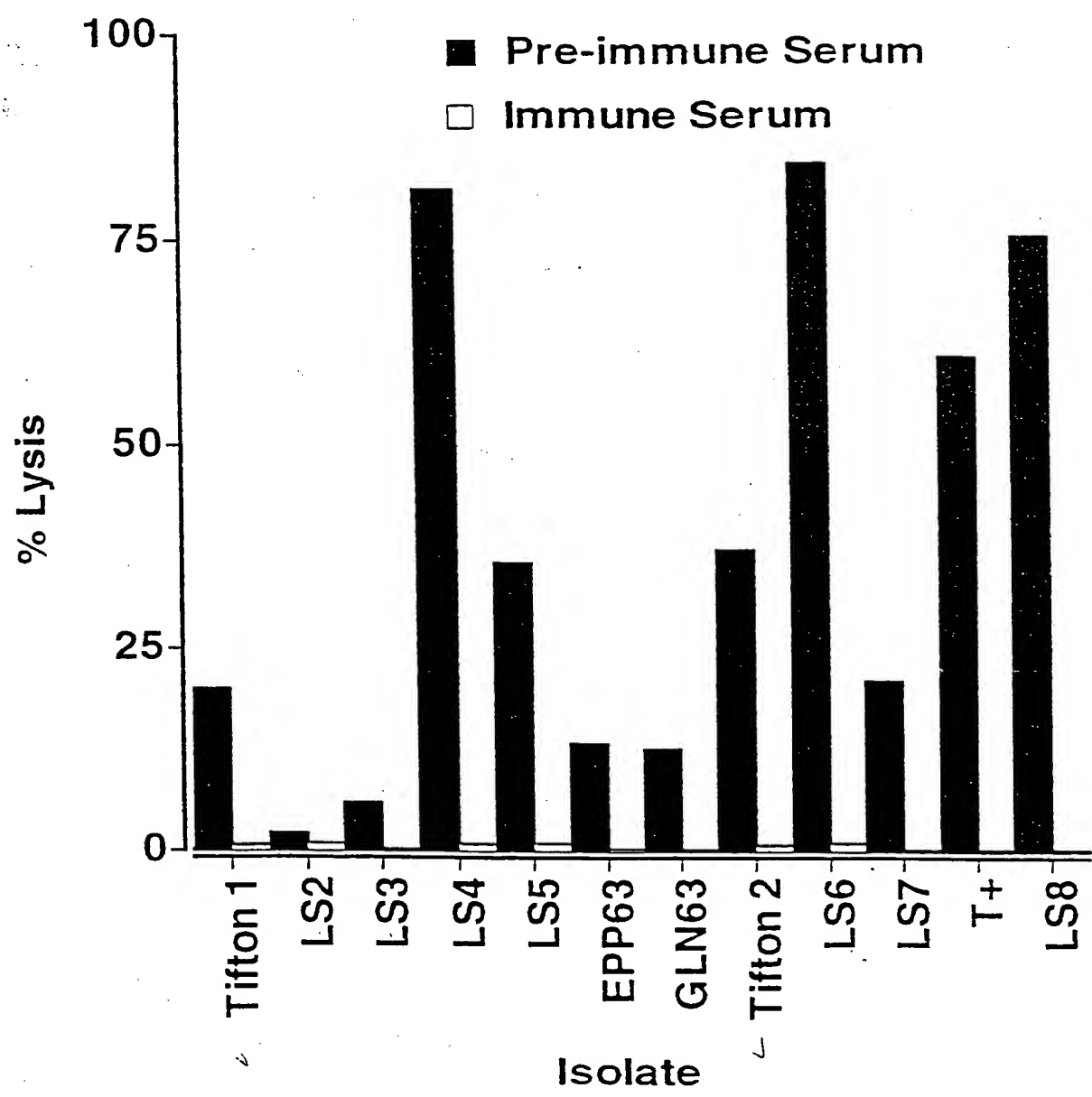


FIG. 2

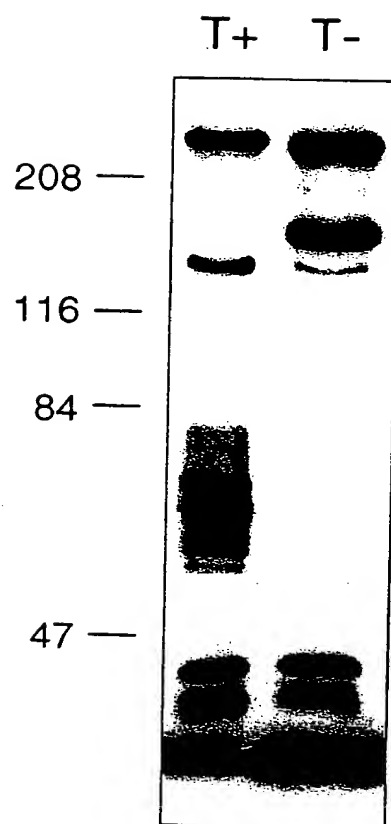


FIG 3-1

Appendix A update-July 1999

Bases 1-1200

Amino acids 1-400

1	ATGTCCAATATAAATGTAATTAATCTAATATTCAAGCAGGCTTGAATTCAACAAAGTCT	60
1	M S N I N V I K S N I Q A G L N S T K S	20
61	GGATTAATAAATCTTTACTTGGCTATTCCCAAAGATTATGATCCGCAAAAAGGTGGGACT	120
21	G L K N L Y L A I P K D Y D P Q K G G T	40
121	TTAAATGATTTTATTAAGCTGCTGATGAATTAGGTATTGCTCGTTTAGCAGAAGAGCCT	180
41	L N D F I K A A D E L G I A R L A E E P	60
181	AATCACACTGAAACAGCAAAAAAATCTGTTGACACAGTAAATCAGTTTCTCTCTCTCACA	240
61	N H T E T A K K S V D T V N Q F L S L T	80
241	CAAACTGGTATTGCTATTTCTGCAACAAAATTAGAAAAGTTCTTACAAAAACATTCTACC	300
81	Q T G I A I S A T K L E K F L Q K H S T	100
301	AATAAGTTAGCCAAAGGGTTAGACAGTGTAGAAAATATTGATCGTAAATTAGGTAAAGCA	360
101	N K L A K G L D S V E N I D R K L G K A	120
361	AGTAATGTATTATCAACATTAAGCTCTTTTTTGGGCACTGCATTAGCGGGTATAGAAGT	420
121	S N V L S T L S S F L G T A L A G I E L	140
421	GATTCTTTAATCAAAAAAGGTGATGCTGCACCTGATGCTTTGGCTAAAGCTAGTATTGAC	480
141	D S L I K K G D A A P D A L A K A S I D	160
481	TTGATTAATGAGATAATTGGTAATCTATCTCAGAGTACTCAAACGATTGAAGCATTTTCT	540
161	L I N E I I G N L S Q S T Q T I E A F S	180
541	TCACAGTTAGCAAAGTTAGGTTCTACTATATCGCAGGCTAAAGGCTTCTCTAATATAGGA	600
181	S Q L A K L G S T I S Q A K G F S N I G	200
601	AACAAGTTGCAAACTTAAATTTTTCTAAAACAAATCTTGGTTTGGAAATAATTACTGGT	660
201	N K L Q N L N F S K T N L G L E I I T G	220
661	TTGCTATCAGGCATTTCTGCAGGCTTTGCTTTAGCGGATAAAAAATGCATCGACTGGCAAA	720
221	L L S G I S A G F A L A D K N A S T G K	240
721	AAAGTTGCTGCAGGTTTTGAATTAAGCAATCAAGTTATTGGTAATGTAACAAAGCAATT	780
241	K V A A G F E L S N Q V I G N V T K A I	260
781	TCTTCATATGTTTTAGCACACGTGTTGCTGCTGGTCTATCAACTACTGGTGCTGTTGCT	840
261	S S Y V L A Q R V A A G L S T T G A V A	280
841	GCTTTAATTACTTCATCGATTATGTTGGCAATTAGTCCTTTGGCATTATGAATGCAGCA	900
281	A L I T S S I M L A I S P L A F M N A A	300
901	GATAAATTCATCATGCTAATGCTCTTGATGAGTTTGCAAAACAATCCGAAAATTTGGC	960
301	D K F N H A N A L D E F A K Q F R K F G	320
961	TATGATGGGGATCATTTATTGGCTGAATATCAGCGTGGTGTGGGTACTATTGAAGCTTCA	1020
321	Y D G D H L L A E Y Q R G V G T I E A S	340
1021	TTAACTACAATTAGTACGGCATTAGGTGCAGTTTCTGCTGGTGTTCGCTGCTGCTGTA	1080
341	L T T I S T A L G A V S A G V S A A A V	360
1081	GGATCTGCTGTTGGTGCACCGATTGCACTATTAGTTGCAGGTGTTACAGGATTGATCTCT	1140
361	G S A V G A P I A L L V A G V T G L I S	380
1141	GGAATTTTAGAAGCGTCTAAACAGGCAATGTTTGAAAGTGTTGCTAACCGTTTACAAGGT	1200
381	G I L E A S K Q A M F E S V A N R L Q G	400

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FIG 3-3

Appendix A update-July 1999, continued

Bases 2401-2784

Amino acids 801-927

2401	GGTATTATAGTTAAACGAAATGATCATTCAAGTAGTATTAACATACCAAGATGGTACATA	2460
801	G I I V K R N D H S G S I N I P R W Y I	820
2461	ACATCAAATTTACAAAATTATCAAAGTAATAAAACAGATCATAAAATTGAGCAACTAATT	2520
821	T S N L Q N Y Q S N K T D H K I E Q L I	840
2521	GGTAAAGATGGTAGTTATATCACTTCCGATCAAATTGATAAAATTTTGCAAGATAAGAAA	2580
841	G K D G S Y I T S D Q I D K I L Q D K K	860
2581	GATGGTACAGTAATTACATCTCAAGAATTGAAAAAGCTTGCTGATGAGAATAAGAGCCAA	2640
861	D G T V I T S Q E L K K L A D E N K S Q	880
2641	AAATTATCTGCTTCGGACATTGCAAGTAGCTTAAATAAGCTAGTTGGGTCAATGGCACTA	2700
881	K L S A S D I A S S L N K L V G S M A L	900
2701	TTTGGTACAGCAAATAGTGTGAGTTCTAACGCCTTACAGCCAATTACACAACCAACTCAA	2760
901	F G T A N S V S S N A L Q P I T Q P T Q	920
2761	GGAATTTTGGCTCCAAGTGTITAG	2784
921	G I L A P S V *	928

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SEQ ID NO: 2

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[illegible][illegible]

FIG. 5

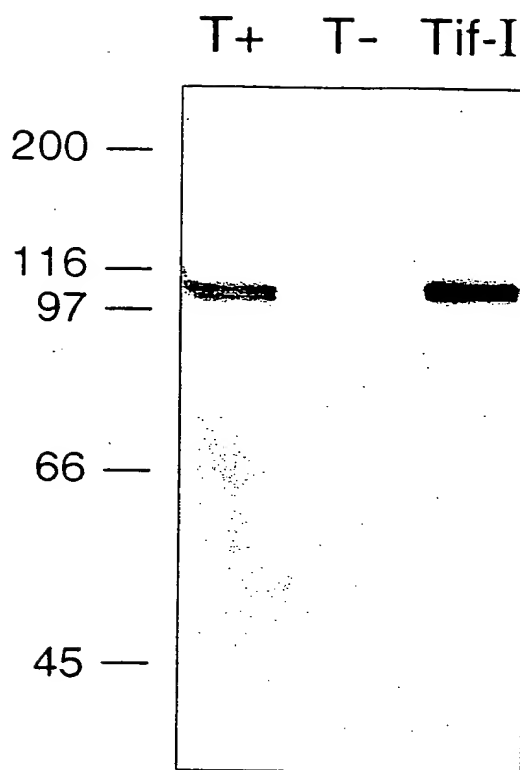
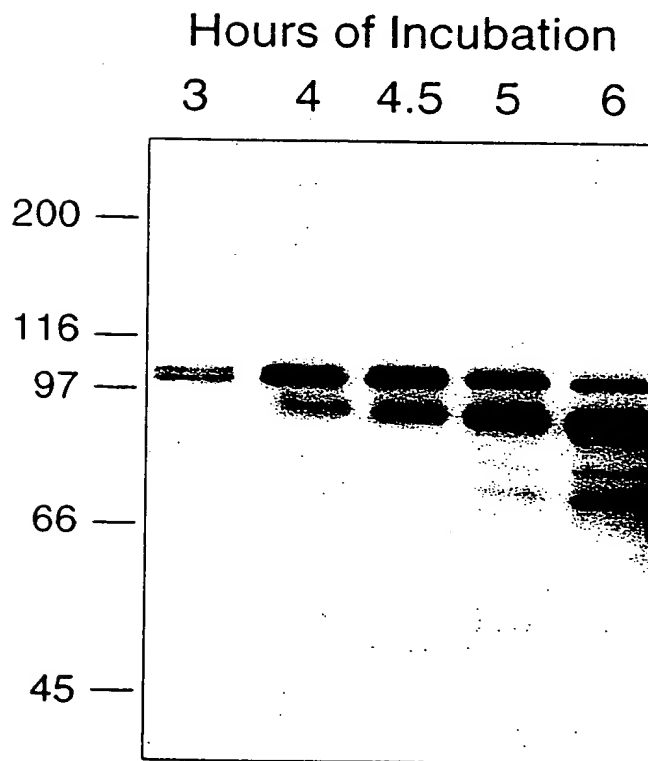
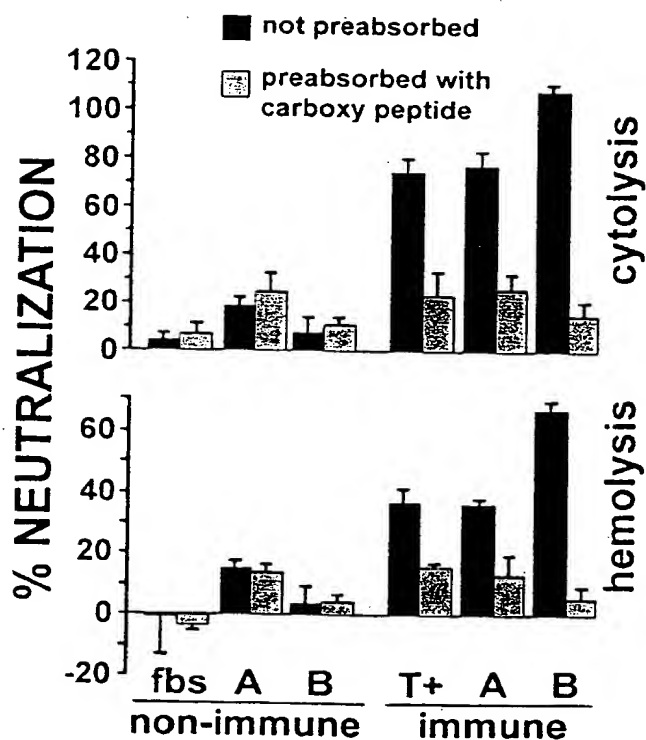


FIG. 6



F16.7



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UNASIS TRANSLATION EDITOR [11-00 B gene.uno]

1	ATGGGTGGTGATACCTCTTTAATTAGACTTAATTTACAAACCCTTAATAGTAATTTAGTT	60
1	M G G D T S L I R N L Q T L N S N L V	
61	ATGATAGATTATGCTCAACAACCTGCTCTATCTGCTCTGGTTATCCTTGCCAAATACTAT	120
21	M I D Y A Q Q P A L S A L V I L A K Y Y	40
121	GGTATTTCTGCAAGTCCAGCAGACATTATGCATCAGTTTTCTGATAATACAAAAGGAGAC	180
41	G I S A S P A D I M H Q F S D N T K G D	60
181	CTGAATGAAATTGAATGGATGTTGGCAGCAAAGAAATTAGAATTAAAGGTAAAGATTATA	240
61	L N E I E W M L A A K K L E L K V K I I	80
241	AAACAGCCTTTAACTCGATTGTCAATGATAACACTTCTGCTTTGGTGTGGTGTGATAAT	300
81	K Q P L T R L S M I T L P A L V W C D N	100
301	AAGCCCGATTTAGATCAAAATTTAACTCTCATTTTATACTAACTAAAATTGATGGGGTG	360
101	K P D L D Q N L N S H F I L T K I D G V	120
361	GGATCTGCTGCAAAATATCTCATCTACGATTTGATTGAGAATCGTCCCATAATATTAGAT	420
121	G S A A K Y L I Y D L I E N R P I I L D	140
421	GCAAGTGAGTTTTCTGAAAGATATTCTGGTAAGTTAATGCTAGTAACTTCCCGTGCGTCA	480
141	A S E F S E R Y S G K L M L V T S R A S	160
481	ATATTGGGTTTCATTGGCTAAATTTGATTTTACTTGGTTTATCTGCGGTAATCAAATAT	540
161	I L G S L A K F D F T W F I P A V I K Y	180
541	CGTTATATTTTTTTGAAGTCATCGTTATTTTCAGTGGTGCTACAGATTTTTGCTCTGATT	600
181	R Y I F F E V I V I S V V L Q I F A L I	200
601	ACGCCATTGTTTTTTCAGGTTGTGATGGATAAGGTATTGGTGCATCGTGGTTTTTCTACT	660
201	T P L F F Q V V M D K V L V H R G F S T	220
661	CTGGATGTGGTAGCGATTGCCTTGTGGTAGTAAGTTTATTTGAAGTCATTTTAAGTGGT	720
221	L D V V A I A L L V V S L F E V I L S G	240
721	CTACGCACTTATTTTTGCTCATACAACCTCTCGAATTGATGTAGAGCTAGGAGCACGA	780
241	L R T Y I F A H T T S R I D V E L G A R	260
781	TTATTTTCGTCATCTATTAGCTCTACCGCTTGCTTATTTTGAGAGTAGAAGAGTAGGCGAT	840
261	L F R H L L A L P L A Y F E S R R V G D	280
841	ACAGTTGCACGTATACGTGAATTGGAACATATCCGCAATTTCTTAACTGGTCAAGCTCTC	900
281	T V A R I R E L E H I R N F L T G Q A L	300
901	ACTTCAGTTTTAGATTTGGTGTCTTTTATATTCTTGTTTGTAATGTGGTATTACAGC	960
301	T S V L D L V F S F I F L F V M W Y Y S	320
961	CCTACTTTAACTGGTAGTTTTGGCATCATTACCAATATATGCGTTTTGGTCTGCCTTT	1020
321	P T L T L V V L A S L P I Y A F W S A F	340
1021	ATTAGCCCAATTTTACGCACTCGACTAAATGATCAATTTGCACGCAATGCAGATAATCAA	1080
341	I S P I L R T R L N D Q F A R N A D N Q	360
1081	TCTTTTTTAGTGGAAGTATTACTGCGTTGGTACGGTAAAAGCAATGGCAGTTGAACCT	1140
361	S F L V E S I T A V G T V K A M A V E P	380
1141	CAAATGACCCGTCGCTGGGATAATCAATTAGCAGCTTATGTGGTTTCTAGTTTTCGGGTA	1200
381	Q M T R R W D N Q L A A Y V V S S F R V	400
1201	GCTAAGTTGGCAATGGTTGGGCGCAAGGAGTACAACCTCATTCAAAAGATGGTTATTGTG	1260
401	A K L A M V G Q Q G V Q L I Q K M V I V	420
1261	GCAACTCTATGGATTGGTGCAAAATTGGTAATTGAAGGCAAGCTATCGGTAGGTCAATTA	1320
421	A T L W I G A K L V I E G K L S V G Q L	440

8-1
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DNASIS TRANSCRIPTION ERROR [11-00 0 gene.000]

1321	ATAGCATTTAATATGCTGGCAGGTCAGGTGGCCGCTCCTGTTATCCGCCTGGCACAGCTA	1380
441	I A F N M L A G Q A A P V I R L A Q L	
1381	TGGCAAGATTTTCAGCAAGTAGGTATTTTCAGTGGCGAGATTGGGTGATATTTTAAATACT	1440
461	W Q D F Q Q V G I S V A R L G D I L N T	480
1441	CCAACTGAGCATTCTACATCTCGCTTAACCTTTACCTGATATTAAGGGTGATATTACATTT	1500
481	P T E H S T S R L T L P D I K G D I T F	500
1501	GAAATGTTGATTTTCGCTACAAAATAGATGGGCATTTAATATTACAGAATTTAAATTTA	1560
501	E N V D F R Y K I D G H L I L Q N L N L	520
1561	CAGATTAACGCTGGAGAGATACTAGGTATCGTAGGACGCTCTGGTTCAGGTAAATCAACA	1620
521	Q I N A G E I L G I V G R S G S G K S T	540
1621	TTGACAAAATTAGTAAEAGCGTTTATATGTACCAGAAAATGGGCGAATATTAGTTGATGGA	1680
541	L T K L V Q R L Y V P E N G R I L V D G	560
1681	AACGATTTGGCATTAGCTGATCCCGCTTGGCTGCGTCGCCAAGTGGGTGTTGTTTTGCAG	1740
561	N D L A L A D P A W L R R Q V G V V L Q	580
1741	GAAAATGTGTTACTCAATCGTAGTATTCGAGATAATATTGCCCTAACTGATACGGGCATG	1800
581	E N V L L N R S I R D N I A L T D T G M	600
1801	TCATTAGAGTTTATTATCCAGGCTGCCAAGATGTCTGGGGCACATGACTTTATTATGGAA	1860
601	S L E F I I Q A A K M S G A H D F I M E	620
1861	TTGCCTGAGGGTTATGATACGATTGTTGGAGAGCAAGGTGCAGGCTTGTGAGGTGGACAA	1920
621	L P E G Y D T I V G E Q G A G L S G G Q	640
1921	CGCCAGCGTATCGCTATTGCGCGTGCTTTAATTACCAATCCGCGTATTTTGATTTTGTAT	1980
641	R Q R I A I A R A L I T N P R I L I F D	660
1981	GAAGCTACTAGTGCATTAGACTATGAGTCGGAAAGGGCTATTATGCAAAATATGCAGGCA	2040
661	E A T S A L D Y E S E R A I M Q N M Q A	680
2041	ATTTGCCAAGGTAGAACAGTGTTGATTATTGCACATCGCTTATCTACCGTAAAAATGGCA	2100
681	I C Q G R T V L I I A H R L S T V K M A	700
2101	CATCGCATTATTGCAATGGACAAGGGGAAAATTGTAGAGCAAGGCACACATCAAGAATTG	2160
701	H R I I A M D K G K I V E Q G T H Q E L	720
2161	TTGCAAAAAGAAGATGGTTACTATCGTTATTTATATGATTTGCAGAATGGATAAA	2215
721	L Q K E D G Y Y R Y L Y D L Q N G *	739

F16.8-2

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F15.9

MbxB	---	MED	LAQPPALSA	LVILAKVCG	ISASPAIM	HQPSDNTK	DLNEISW	AAKKLSL	55		
LktB	M	ANQ	GLVA	LTHLAQYBN	ISLEPERIM	HKPDLGKGC	LSLTAWLL	AAKSLAL	56		
ApXIB	MDF	YRE	GLYA	LTILAQYBN	IAVPPSEK	HKVDLCKGC	LDLTAWLL	AAKSLAL	55		
HlyB	MDS	CHK	GLYA	LEILAQYBN	ISVPPSEK	HKPDTGKGC	LGLTAWLL	AAKSLAL	55		
MbxB	RVK	IKOP	TALSMITLP	ALVWCNDKP	DLDQNLNSB	FILTKIDGV	GSAAKYLIV	DLINRPF	116		
LktB	KAR	IKET	SRLHLNLP	ALVWQDN	FLVRVD	TNNRKLIV	NLEGDAP	107		
ApXIB	KAR	QVKNAT	DRENFIALP	ALVWRED	FILTKID	NEAKKLIV	DLEGRNP	106		
HlyB	KVR	QVKNAT	DRENFIALP	ALVWRED	FILTKID	NEAKKLIV	DLEGRNP	106		
MbxB	IIL	ASEPS	ERYSGRLML	VTSRASVVG	SLAKPDFTW	PIPAVIRYR	YIPFVIV	SVVLQIF	177		
LktB	QIL	STDEPS	MCYQCOLIL	VTSRASVVG	QLAKPDFTW	PIPAVIRYR	KIPFSTLIV	SIPLOIF	168		
ApXIB	RILEQ	ASEPS	SLYQGRILIL	VASRASVVG	KLAKPDFTW	PIPAVIRYR	KIPFSTLIV	SIPLOIF	167		
HlyB	R	LEQSEPS	ALYQCHIL	VASRASVVG	KLAKPDFTW	PIPAVIRYR	KIPFSTLIV	SIPLOIF	167		
MbxB	ALITPLFPQ	VVMKRVLVH	RCFSTLDV	A	ALLVVS	FR	LSGLR	TYIFAHST	RIDVELG	238	
LktB	ALITPLFPQ	VVMKRVLVH	RCFSTLDV	A	ALLVVS	FR	LSGLR	TYIFAHST	RIDVELG	229	
ApXIB	ALITPLFPQ	VVMKRVLVH	RCFSTLDV	A	ALLVVS	FR	LSGLR	TYIFAHST	RIDVELG	228	
HlyB	ALITPLFPQ	VVMKRVLVH	RCFSTLDV	A	ALLVVS	FR	LSGLR	TYIFAHST	RIDVELG	228	
MbxB	ARLPRHLLA	LPAYFESR	RVGDTVARV	REL	MIRNP	LTCOALTSV	LDLVFSFIF	LFVMWYF	299		
LktB	AKLPRHLLS	LPISYFENR	RVGDTVARV	REL	DOIREP	LTCOALTSV	LDLVFSFIF	FVMWYF	290		
ApXIB	AKLPRHLLA	LPISYFESR	RVGDTVARV	REL	DOIREP	LTCOALTSV	LDLVFSFIF	FVMWYF	289		
HlyB	AKLPRHLLA	LPISYFESR	RVGDTVARV	REL	DOIREP	LTCOALTSV	LDLVFSFIF	FVMWYF	289		
MbxB	SPKLTTLVL	L	ASLPITAFW	SAFISPIRL	TRLNDQFAR	HADNQSPLV	ES	TA	GT	KAMAV	360
LktB	SPKLTTLVL	L	ASLPITAFW	SAFISPIRL	TRLNDQFAR	HADNQSPLV	ES	TA	GT	KAMAV	351
ApXIB	SPKLTTLVL	L	ASLPITAFW	SAFISPIRL	TRLNDQFAR	HADNQSPLV	ES	TA	GT	KAMAV	350
HlyB	SPKLTTLVL	L	ASLPITAFW	SAFISPIRL	TRLNDQFAR	HADNQSPLV	ES	TA	GT	KAMAV	350
MbxB	QNTRRWDNQ	LAATVVS	SSP	RVARLAM	G	QGGVQLIQ	MVIVATLW	GAKLVIEGK	LS	GOLI	421
LktB	QNTTWDNQ	LAATVVS	SSP	RVARLAM	G	QGGVQLIQ	MVIVATLW	GAKLVIEGK	LS	GOLI	412
ApXIB	QNTTWDNQ	LAATVVS	SSP	RVARLAM	G	QGGVQLIQ	MVIVATLW	GAKLVIEGK	LS	GOLI	411
HlyB	QNTTWDNQ	LAATVVS	SSP	RVARLAM	G	QGGVQLIQ	MVIVATLW	GAKLVIEGK	LS	GOLI	411
MbxB	AFNMLAGOV	AAPVIRLAQ	LWQDFQOVG	ISVARLGDV	LSPTESYH	LSPTESYH	LSPTESYH	LSPTESYH	LSPTESYH	LSPTESYH	482
LktB	AFNMLAGOV	AAPVIRLAQ	LWQDFQOVG	ISVARLGDV	LSPTESYH	LSPTESYH	LSPTESYH	LSPTESYH	LSPTESYH	LSPTESYH	473
ApXIB	AFNMLAGOV	AAPVIRLAQ	LWQDFQOVG	ISVARLGDV	LSPTESYH	LSPTESYH	LSPTESYH	LSPTESYH	LSPTESYH	LSPTESYH	472
HlyB	AFNMLAGOV	AAPVIRLAQ	LWQDFQOVG	ISVARLGDV	LSPTESYH	LSPTESYH	LSPTESYH	LSPTESYH	LSPTESYH	LSPTESYH	472
MbxB	DPRIKIDG	HLILQNL	QENAGE	IVGRSGSGK	STLTLLOR	LYPENGRT	L	DGNL	543		
LktB	IPRIKIDG	HLILQNL	QENAGE	IVGRSGSGK	STLTLLOR	LYPENGRT	L	DGNL	534		
ApXIB	IPRIKIDG	HLILQNL	QENAGE	IVGRSGSGK	STLTLLOR	LYPENGRT	L	DGNL	533		
HlyB	IPRIKIDG	HLILQNL	QENAGE	IVGRSGSGK	STLTLLOR	LYPENGRT	L	DGNL	533		
MbxB	ALADPANLR	ROVGVVLQD	HVLLERSIR	DNIALTDIG	MS	EF	IAQA	AKLAGADP	IMELREG	604	
LktB	ALADPANLR	ROVGVVLQD	HVLLERSIR	DNIALTDIG	MS	EF	IAQA	AKLAGADP	IMELREG	595	
ApXIB	ALADPANLR	ROVGVVLQD	HVLLERSIR	DNIALTDIG	MS	EF	IAQA	AKLAGADP	IMELREG	594	
HlyB	ALADPANLR	ROVGVVLQD	HVLLERSIR	DNIALTDIG	MS	EF	IAQA	AKLAGADP	IMELREG	594	
MbxB	NDTIVGEOG	AGLSGGOQO	RIATARALV	TNP	ILIPD	RATSALDYE	SEIRAIM	QNM	QAIC	QGR	665
LktB	NDTIVGEOG	AGLSGGOQO	RIATARALV	TNP	ILIPD	RATSALDYE	SEIRAIM	QNM	QAIC	QGR	656
ApXIB	NDTIVGEOG	AGLSGGOQO	RIATARALV	TNP	ILIPD	RATSALDYE	SEIRAIM	QNM	QAIC	QGR	655
HlyB	NDTIVGEOG	AGLSGGOQO	RIATARALV	TNP	ILIPD	RATSALDYE	SEIRAIM	QNM	QAIC	QGR	655
MbxB	TV	IIAHRL	STVRMAHRI	IAMEGKIV	EQGTHQELL	QKEDGYTRY	LYDLQNG	717	SEIDNO:18		
LktB	TV	IIAHRL	STVRMAHRI	IAMEGKIV	EQGTHQELL	QKEDGYTRY	LYDLQNG	708	SEIDNO:19		
ApXIB	TV	IIAHRL	STVRMAHRI	IAMEGKIV	EQGTHQELL	QKEDGYTRY	LYDLQNG	707	SEIDNO:20		
HlyB	TV	IIAHRL	STVRMAHRI	IAMEGKIV	EQGTHQELL	QKEDGYTRY	LYDLQNG	707	SEIDNO:21		

SEIDNO:18
SEIDNO:19
SEIDNO:20
SEIDNO:21

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FIG. 10

DNASIS Translation Editor [11-00 C gene.dna]

1	ATGACGAAAAAGTTTGCAGAGCTAGGTTTAATTGCATGGCTTTGGTCTAACTCTGATATG	60
1	M T K K F A E L G L I A W L W S N S D M	20
61	CATAAACATTGGACGTTGTCTTTGTTTGCACCAATGTTATCCGGCAATTGAGACAGGT	120
21	H K H W T L S L F A T N V I P A I E T G	40
121	CAATATGTTATATTGAAAAGAGAAGATATGCCTGTAGCATATTGTAGTTGGGCTAAACTT	180
41	Q Y V I L K R E D M P V A Y C S W A K L	60
181	AGTTTAGAAAACGAGGTTAAATATATTAACGATGTTACTTCTCTTAAGTTAGATGACTGG	240
61	S L E N E V K Y I N D V T S L K L D D W	80
241	CAGTCAGGTGACCGAAACTGGTTTATTGACTGGATTGCTCCATTGGCGATAGTCTTACA	300
81	Q S G D R N W F I D W I A P F G D S L T	100
301	CTCACAAAACACATGAGAACGTTATTTTCAGATGAATTGTTTAGAGCGATTCTGTGTAGAT	360
101	L T K H M R T L F S D E L F R A I R V D	120
361	GGAAATTCATCGCATGGTAAGATATCTGAATTTTATGGAAAGTCTGTTGATTCAAAATTA	420
121	G N S S H G K I S E F Y G K S V D S K L	140
421	GCCTCAAGAATATTTGCACAATATCACGAAGATTTGACGAGCAAATTGTCAACTCAGAAT	480
141	A S R I F A Q Y H E D L T S K L S T Q N	160
481	AATTTTATTATATCTAAAGATAATTAA	507
161	N F I I S K D N *	169

mbx C
Mbx C

FIG. 11

MbxC	- - - M T K K F A E	L G L I A W L W S N	S D E K H W T L S	L P A T N V I P A I	E T G Q Y	42
LktC	- - - M N Q S Y F N L	L G N I T W L W M N	S S L E K E W S C E	L L A R N V I P A I	E N E Q Y	43
ApXIC	M S K K I N G F E V	L G E V A W L W A S	S P L E R K W P L S	L L A I N V L P A I	E S N Q Y	45
HlyC	- M N R N N P L E V	L G H V S W L W A S	S P L E R N W P V S	L P A I N V L P A I	R A N Q Y	44

MbxC	V L K R E D M P V	A Y C S W A K L S L	E N E V K Y I N D V	T S L K L D D W Q S	G D R N W	87
LktC	M L L I D N G I P I	A Y C S W A D L N L	E T E V K Y I N D V	N S L T P E R W Q S	G D R R W	88
ApXIC	V L L K R D G F P I	A Y C S W A N L N L	E N E I K Y L D D V	A S L V A D D W T S	G D R R W	90
HlyC	A L L T R D N Y P V	A Y C S W A N L S L	E N E I K Y L N D V	T S L V A E D W T S	G D R W	89

MbxC	F I D W I A P F G D	S L T L T K H M R T	L F S D E L F R A I	R V D G N S S . H G	K I S E F	131
LktC	I I D W I A P F G H	S Q L L Y K K M C Q	K P D M T V R S I	R F Y P K O K E L G	K I A Y F	133
ApXIC	F I D W I A P F G D	S A A L Y K H M R D	N F P N E L F R A I	R V D P D S R . V G	K I S E F	134
HlyC	F I V W I A P F G D	N G A L Y K M R K	K P P D E L F R A I	R V D P K T H . V G	K I S E F	133

MbxC	H G K S V D S K L A	S I F A Q Y H E E	L T S K L S T Q N N	F I I S K D N -	168
LktC	K G G K I D K R T A	K R R R F D T Y Q E E	L A T A L K N E F N	F I K K - - -	167
ApXIC	H G G K I D K R L A	S K I F Q Q Y H F E	L M S E L K N K Q N	F K F S L V N S	172
HlyC	H G G K I D K R L A	N K I P K Q Y H E E	L I T E V K N K S D	F N F S L T G -	170

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1 M F I Q A L K D F I R Y I T V W R N T

61 TGGGCAGTTCGAGACCACTAACCCTCTAAGCGTACTAAAGAAGAACTCGCTTTTCTT 120
21 W A V R D Q L T P P K R T K E E L A F L 40

121 CCTGCACATCTAGAACTCACTGACACACCTGTATCCAGATCTTCTAAGTGGACAGCTAGA 180
41 P A H L E L T D T P V S R S S K W T A R 60

181 ATAATCATGATATTTGCTCTATTTGCTTTGCTATGGTCTTGGGTGGACAGATTGACATT 240
61 I I M I F V L F A L L W S W V G Q I D I 80

241 GTTGCTACAGCTTCAGGTAAAATTTCTTCAGGTAGCCGTAGCAAGACTATTCAATCTTTG 300
81 V A T A S G K I S S G S R S K T I Q S L 100

301 GAAACAGCGATAGTTAAAGCAGTTTATGTACGTGATGGTCAAAATGTTCAACAAGGTGAA 360
101 E T A I V K A V Y V R D G Q N V Q Q G E 120

361 ATATTAGTAGATTTAGTGGGAATCGGTTCAAGATAGTGATGTTGCTCAGTCCGAGAAAGCC 420
121 I L V D L V G I G S D S D V A Q S E K A 140

421 CTTGAGCAGCGCAATTATCTAAGCTACGCCTTGAAGCAATTTTATCAGCATTAAATCAC 480
141 L R A A Q L S K L R L E A I L S A L N H 160

481 CGTATTAATCCTCAGATTGATGTAGCATATGCAAAGTCTTTAAATATTTTCAAGATCGGAA 540
161 R I N P Q I D V A Y A K S L N I S E S E 180

541 ATTAATGAAGCTCAAACTTTAGCCCAAAATCAATATCAAGCATGGTTAGCACAAGATGAA 600
181 I N E A Q T L A Q N Q Y Q A W L A Q D E 200

601 CAACTAAAATTAACCTTAAAAGGACATCAAGCAGAATTACAATCTGCTCGATCCCAAGAA 660
201 Q L K L T L K G H Q A E L Q S A R S Q E 220

661 CAAAAGTTGGTTTCAGTTGGTGCAATTGAACATCAAAAGACTGATGATTATCGGAGTCTC 720
221 Q K L V S V G A I E H Q K T D D Y R S L 240

721 AAAGCAGAAAAATTTTATATCTGAGCATGCTTATCTAGAACAAGAAAGCAAATTAAGC 780
241 K A E N F I S E H A Y L E Q E S K L L S 260

781 AATCAAAATGATTTACAAAGTACACGTAGTCAGATTCAAAAAATACAGGCTGCAATCATG 840
261 N Q N D L Q S T R S Q I Q K I Q A A I M 280

841 CAAGCTGAACAGAACCGTATGTTATATACTCAAAATCTAAACGTGATACATTAGAATCT 900
281 Q A E Q N R M L Y T Q N L K R D T L E S 300

901 TTACGCCAAACCAATGAACAGATTAATCAATATACTGGTCAAACCTAATAAGCTAAGCAG 960
301 L R Q T N E Q I N Q Y T G Q T N K A K Q 320

961 CGACAGAAATTGCTGAGTATTAATCACCTGTTAATGGTACTATACAAGAGCTAACAGCT 1020
321 R Q K L L S I K S P V N G T I Q E L T A 340

1021 TATACTTTAGGTGGAGTTGTACAAGCAGCACAAAAAATTATGGTTGTGGCACCTAACGAT 1080
341 Y T L G G V V Q A A Q K I M V V A P N D 360

1081 AATCAAGTGAAGTAGAGGTATTAGTGCTAAATAAGATATCGGCTTTGTAAGCTGGG 1140
361 N Q V E V E V L V L N K D I G F V K A G 380

1141 CAGAATGTTATCATCAAAATCGAGAGTTTTCTTATACACGTTATGGTTATTTAACAGGT 1200
381 Q N V I I K I E S F P Y T R Y G Y L T G 400

1201 AAAATAAAAAGTATTAGTCATGATGCTATAGAACATCAACATTTAGGTCTAGTGATACT 1260
401 K I K S I S H D A I E H Q H L G L V Y T 420

1261 GCACTTGTCTCTTGTATAAAAGCACATTAATATAGATGGAGTAACAATCAACTTAACG 1320
421 A L V S L D K S T L N I D G V T I N L T 440

60 F1612-1

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UNASIS TRANSLATION ERROR L11-00 0 gene.0000

1321 CCAGGAATGAATGTTACTGCTGAAATTTAAACAGGTAAACGTCGTGTTTTGGATTATATA 1380
441 P G M N V T A E I T G K R R V L D Y I

1381 TTAAGTCCATTGCAGACAAAAGTTGATGAAAGTTTTGAGAACGCTAA 1428
461 L S P L Q T K V D E S F R E R * 476

FIG. 12-2

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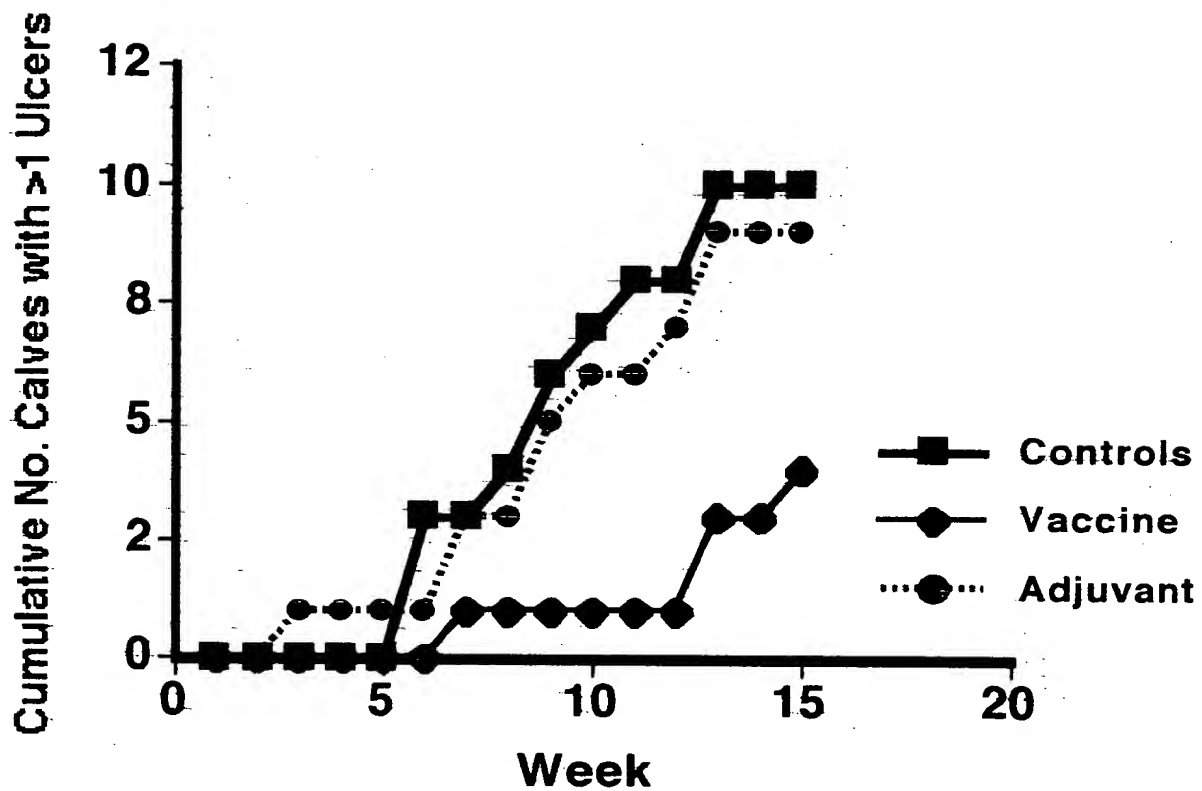
FIG. 13

MbxD	--MF--QALK	FFRYITVWR	NTWARDQLT	PPKRTKELA	FLPAHLELT	48
LktD	MRIWLSG	FFLRYKNWA	EVWKRRLD	HPNRKRDESE	FLPAHLELIE	50
ApxD	MKTWLMGLYE	FFQRYKTVWT	EINRIRHOLD	TPDRERDENE	FLPAHLELIE	50
HlyD	MKTWLMGFSE	FLRLRYKLVWS	ETWKRIRKQLD	TPVVRERDENE	FLPAHLELIE	50
MbxD	TPVSRSSWT	ARIMFVLF	ALLNSWVGQ	IVATASGKL	SSGSRSKTIQ	98
LktD	TPVSKKPRLI	AYLIMLPLVV	AVLASVSKV	EIVATAPGKL	TFSGRSKEIR	100
ApxD	TPVSKKPRLI	AYLIMLPLFL	ALVSIIVSHV	EIVATATGKL	AFSDRSKEIR	100
HlyD	TPVSRPRLI	AYFIMGPLVI	APFLSVLGQV	EIVATANGL	TLSGRSKEIR	100
MbxD	SETAIVKA	VVDGQNVQ	GELVDLVG	GSDDVAQSE	KALRAAQLSK	148
LktD	PIENAIVQEI	FVKDGGQFVER	GQLLVSLTAL	GSDDADIKKTM	ASLSLAKLEN	150
ApxD	PIENAIVKEI	FVQDGGQFVER	DQLLLHLTAL	GADADQQRK	SSLSLTKLER	150
HlyD	PIENSIVKEI	IVKGLSVRR	GDVLLKLTAL	GADADTLKTQ	SSLLQAALBQ	150
MbxD	LRLEAALSA	NHRINPOIDV	AYAKSLNIS	ESEINEAQTL	AQNOYQAWLA	197
LktD	YRYQTLLTAI	SKESLPVIDL	SRTEFKDSS	EEDRLRIKHL	IEEQYTTWQR	199
ApxD	YRYETLLLEA	AADRLPLIL	TKDEFKHA	EEDKTRIRYL	ITEQFEAWQR	199
HlyD	TRYQILSRIS	ELNKLPEKL	PDEPYFQNV	EDEVLRITSL	IKEQFSTWQN	200
MbxD	ODEQLKLT	GHAELQSAR	SQEOKLVSVG	AIEHKTDD	RSLKAENFIS	247
LktD	OKTOKTLLAYK	RKEABKOTIF	AYRRKYEGAT	RIEQEKLLKDF	KALYKQKSIS	249
ApxD	OKYQKELALQ	REABKOTIL	ANIRKYECS	RVENERLKL	KRLFNRSKTS	249
HlyD	OKYQKELNLD	AKRAELTIL	ARINYENVS	RVEKSRLLDDF	RSLLHKQATA	250
MbxD	EHAYLEQESK	LNSQNMLOS	TRSOQKIMIA	AIEQAEENRM	LYTONLKRDT	297
LktD	RHELLAQENK	LIEAQNAAVAV	YRSKLINEEN	DLLNVKEELE	LITOFFKSDI	299
ApxD	KHDVLTQEN	HIEAVNELAV	YKSRLINEES	DLROAKEEIH	LITOLFADI	299
HlyD	KHAVLEQENK	YEAANELRV	YKSQLEIES	ILSAKEEYQ	LITOLFKNMI	300
MbxD	LESRLQTNES	INQYTCTNK	AKQROKLLSI	SPVNGTQ	LTAITLGGVV	347
LktD	LEKLRQHIE	ERQRLRELER	NNORROASMI	RAPVSGTVQ	LKIHTIGGVV	349
ApxD	LEKLRQNVES	EKQLSLELER	NEQROIASVI	RAPVSGTVQ	LKTHTVGGVV	349
HlyD	LKRLRQTTES	IELLTLELER	NEQROQASVI	RAPVSGKVQ	LKVHTEGGVV	350
MbxD	QAAARKMVA	PNDNOVEVEV	LVLNKDIGFV	KAGQNVIIK	ESFPYTRYGY	397
LktD	TTAETLMIV	PEDDDVLEATA	LVPKDKDIFV	AAGQEVIIKV	ETFPYTRYGY	399
ApxD	TTAETLMVIA	PEDDDVLEATA	LQNKDIFGI	EVGQDAIKV	ETFPYTRYGY	399
HlyD	TTAETLMVIV	PEDDDTLEVTA	LVQNKDIFGI	NVQGNATIKV	EAFPYTRYGY	400
MbxD	LTGKIKSISH	DAIEHQHLGL	VTTAEVSD	STLNIDGVT	INTLPGMNV	446
LktD	LTGKIKHISP	DAIEQPNVGL	VPNATIAIDR	KNLTSPDGK	IDLSSGMT	449
ApxD	LMGKVKNITL	DAIEHPQLGL	VPNATIIISDR	KTLSGKDGKE	IELGSSGMT	449
HlyD	LVGKVRKNINL	DAIEDQKLGL	VPNVIVS	NDLSTGNKH	IELGSSGMAVT	449
MbxD	AEIKTGKRRV	EDVLSPLT	KVDESFRER	475	SEDIDNO: 37	
LktD	AEIKTGERSV	MSYLLSPLLE	SVTESLRER	478	SEDIDNO: 38	
ApxD	AEIKTGERSV	ISYLLSPLLE	SVTESLRER	478	SEDIDNO: 39	
HlyD	AEIKTGMRSV	ISYLLSPLLE	SVTESLHER	478	SEDIDNO: 40	

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Cumulative Number of Calves With Severe Ulcers



Number of calves with ulcers with clinical scores $>+2$

FIG 15

Number of calves affected each week

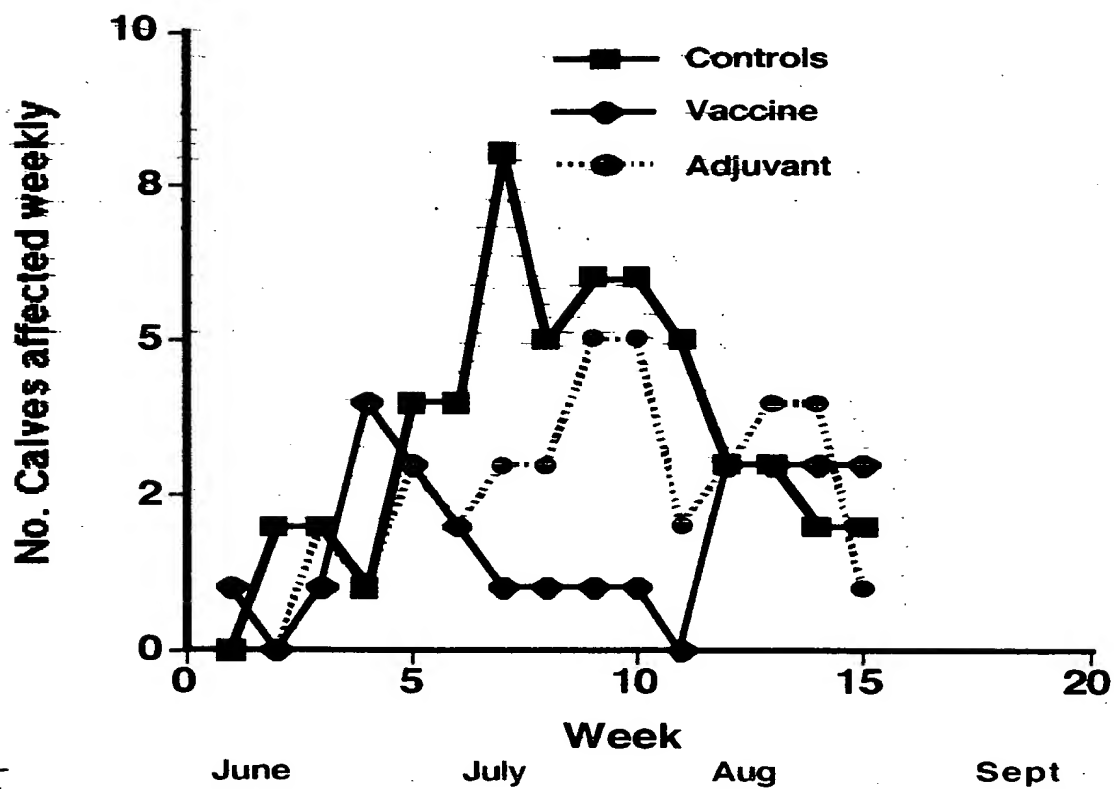
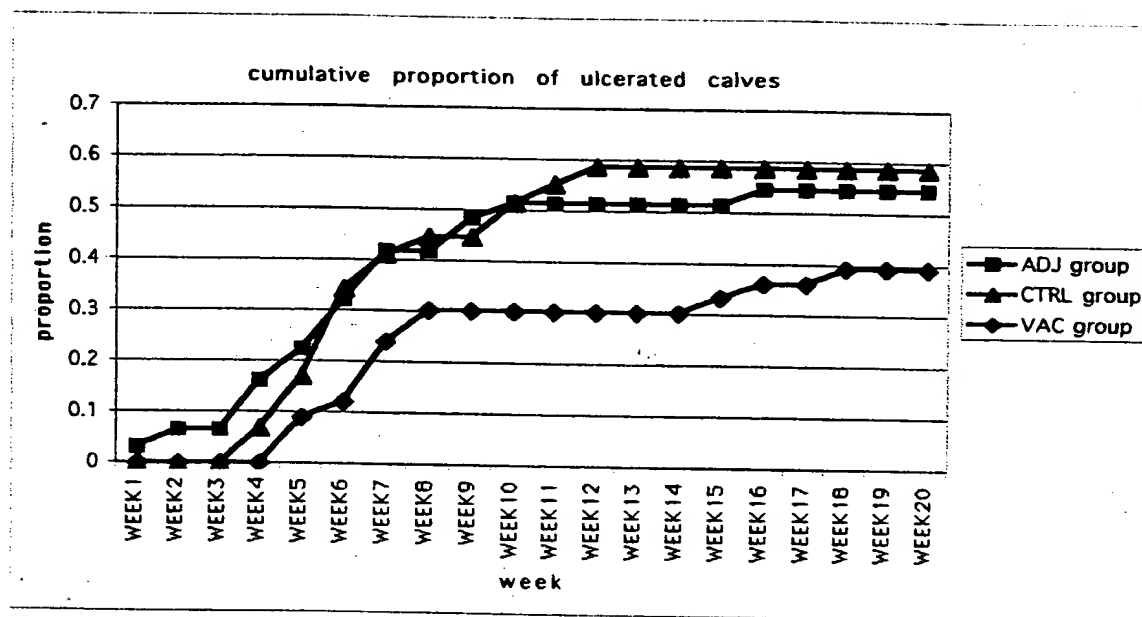


Figure 15
Number of calves affected weekly in 1 group of vaccinated calves and in controls.

FIG. 16



Cumulative proportion of ulcerated calves during the trial. Calves received as vaccines either saline (designated 'CTRL'), adjuvant alone (designated 'ADJ'), or the recombinant cytotoxin vaccine (designated 'VAC').

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